

SEQUENCE LISTING

<110> Cahoon, Rebecca E.
Miao, Guo-Hua
Herrman, Rafael
Rafalski, Antoni
McCutchen, Bill F.

<120> Plant Protein Disulfide Isomerases

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35 40 45

Ala Pro Glu Tyr Glu Glu Ala Ala Thr Thr Leu Lys Glu Lys Asn Ile
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Lys Leu Ala Lys Ile Asp Cys Thr Glu Glu Ser Asp Leu Cys Lys Asp
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Gly Tyr Val Asp Gly Thr Leu Gln Pro Thr Val Lys Ser Glu Glu Ile
35 40 45

Pro Glu Lys Gln Asp Gly Pro Val Tyr Val Leu Val Gly Lys Asn Phe
50 55 60

Glu Ser Ile Val Met Asp Glu Thr Lys Asp Val Leu Val Glu Phe Tyr
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Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Lys Tyr Asp Ala
85 90 95

Leu Gly Glu Ser Phe Lys Ser Asn Pro Asn Val Ile Ile Ala Lys Ile
100 105 110

Asp Ala Thr Ala Asn Asp Thr Pro Val Asp Ile Gln Gly Phe Pro Thr
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Trp Cys Gly His Cys Lys Arg Leu Ala Pro Glu Leu Asp Glu Ala Ala
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Pro Val Leu Ser Gly Leu Ser Glu Pro Ile Val Val Ala Lys Val Asn
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Ala Asp Lys Tyr Arg Lys Leu Gly Ser Lys Tyr Gly Val Asp Gly Phe
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Pro Thr Leu Met Leu Phe Ile His Gly Val Pro Ile Glu Tyr Thr Gly
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Ser Arg Lys Ala Asp Gln Leu Val Arg Asn Leu Lys Lys Phe Val Ser
130 135 140
Pro Asp Val Ser Ile Leu Glu Ser Asp Ser Ala Ile Lys Asn Phe Val
145 150 155 160
Glu Asn Ala Gly Ile Ser Phe Pro Ile Phe Leu Gly Phe Gly Val Asn
165 170 175
Asp Ser Leu Ile Ala Glu Tyr Gly Arg Lys Tyr Lys Lys Arg Ala Trp
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Phe Ala Val Ala Lys Asp Phe Ser Glu Asp Ile Met Val Ala Tyr Glu
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Phe Asp Lys Val Pro Ala Leu Val Ala Ile His Pro Lys Tyr Lys Glu
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Gln Ser Leu Phe Tyr Gly Pro Phe Glu Glu Asn Phe Leu Glu Asp Phe
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Val Arg Gln Ser Leu Leu Pro Leu Val Val Pro Ile Asn Thr Glu Thr
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Glu Asp Asp Ser Asp Glu Asn Ser Thr Gln Leu Val Lys Ile Leu Arg
275 280 285
Ser Ala Ala Asn Ala Asn Arg Asp Leu Val Phe Gly Tyr Val Gly Ile
290 295 300
Lys Gln Trp Asp Gly Phe Val Glu Thr Phe Asp Val Ser Lys Ser Ser
305 310 315 320

Gln Leu Pro Lys Leu Leu Val Trp Asp Arg Asp Glu Glu Tyr Glu Leu
325 330 335

Val Asp Gly Ser Glu Arg Leu Glu Glu Gly Asp Gln Ala Ser Gln Ile
340 345 350

Ser Gln Phe Leu Glu Gly Tyr Arg Ala Gly Arg Thr Thr Lys Lys Lys
355 360 365

Ile Thr Gly Pro Ser Phe Met Gly Phe Leu Asn Ser Leu Val Ser Leu
370 375 380

Asn Ser Leu Tyr Ile Leu Ile Phe Val Ile Ala Leu Leu Phe Val Met
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<212> DNA
<213> Momordica charantia

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 Ala Pro Glu Val Asp Glu Lys Asp Val Val Val Leu Lys Glu Gly Asn
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 Phe Ser Asp Phe Val Glu Lys Asn Arg Phe Val Met Val Glu Phe Tyr
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 Ala Pro Trp Cys Gly His Cys Gln Ala Leu Ala Pro Glu Tyr Ala Ala
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 Ala Ala Thr Glu Leu Lys Gly Glu Asn Val Val Leu Ala Lys Val Asp
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 Ala Thr Glu Glu Asn Glu Leu Ser Gln Lys Tyr Asp Val Gln Gly Phe
 115 120 125
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 Gln Arg Thr Lys Asp Ala Ile Val Thr Trp Ile Lys Lys Lys Ile Gly
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 Thr Ser Glu Thr Lys Val Val Leu Gly Tyr Leu Asn Ser Leu Val Gly
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 Pro Glu Ser Asn Glu Leu Ala Ala Ala Ser Arg Leu Glu Asp Asp Val
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 Asn Phe Tyr Gln Thr Val Asp Pro Glu Val Ala Lys Leu Phe His Ile
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 Glu Ala Ser Ala Lys Arg Pro Ala Leu Val Leu Leu Lys Lys Glu Ala
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 Glu Lys Leu Asn Arg Phe Asp Gly Glu Phe Ser Lys Ser Ala Ile Ala
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 Glu Phe Val Phe Ala Asn Lys Leu Pro Leu Val Thr Lys Phe Thr Arg
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 Glu Ser Ala Pro Leu Ile Phe Glu Ser Ser Ile Lys Lys Gln Leu Ile
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Leu Phe Ala Ile Ser Asn Asp Ser Glu Lys Leu Ile Pro Ile Phe Glu
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 Glu Ser Ser Lys Ser Phe Lys Gly Lys Leu Ile Phe Val Tyr Val Glu
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 Ile Asp Asn Glu Asp Val Gly Lys Pro Val Ser Glu Tyr Phe Gly Ile
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 Ser Gly Asn Gly Pro Glu Val Leu Gly Tyr Thr Gly Asn Glu Asp Ser
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 Lys Lys Phe Val Leu Ala Lys Glu Val Thr Leu Asp Asn Ile Lys Ala
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 Asp Pro Ile Pro Glu Thr Asn Asp Gly Asp Val Lys Val Val Val Gly
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 Asp Asn Phe Asp Asn Ile Val Leu Asp Glu Ser Lys Asp Val Leu Leu
 405 410 415
 Glu Ile Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Glu Pro Thr
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 Tyr Asn Lys Leu Ala Lys His Leu Arg Gly Ile Asp Ser Leu Val Ile
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 Ala Lys Met Asp Gly Thr Thr Asn Glu His Pro Arg Ala Lys Ser Asp
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 Gly Phe Pro Thr Ile Leu Phe Phe Pro Ala Gly Asn Lys Ser Phe Asp
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Ile Pro Thr Asn Asp Pro Asp Gly Trp Pro Glu Gly Asp Tyr Asp Asp
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Asp Asp Leu Leu Phe Gln Asp Gln Asp Gln Asp Leu Thr Gly His Gln
      65              70              75              80
Pro Glu Ile Asp Glu Thr His Val Val Val Leu Ala Ala Ala Asn Phe
      85              90              95
Ser Ser Phe Leu Ala Ser Ser His His Val Met Val Glu Phe Tyr Ala
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Pro Trp Cys Gly His Cys Gln Glu Leu Ala Pro Gly Leu Ser Arg Arg
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 Arg Gly Tyr Asn Gly Ala Arg Thr Lys Glu Ala Ile Val Asp Trp Ile
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 Asn Lys Lys Leu Gly Pro Ala Val Gln Asn Val Thr Ser Val Asp Glu
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 210 215 220
 Asp Thr Leu Ser Gly Ala His Ser Asp Glu Leu Ala Ala Ala Ser Arg
 225 230 235 240
 Leu Glu Asp Ser Ile Asn Phe Tyr Gln Thr Ser Thr Pro Asp Val Ala
 245 250 255
 Lys Leu Phe His Ile Asp Ala Ala Ala Lys Arg Pro Ser Val Val Leu
 260 265 270
 Leu Lys Lys Glu Glu Glu Lys Leu Thr Phe Tyr Asp Gly Glu Phe Lys
 275 280 285
 Ala Ser Ala Ile Ala Gly Phe Val Ser Ala Asn Lys Leu Pro Leu Val
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 Thr Thr Leu Thr Gln Glu Thr Ser Pro Ser Ile Phe Gly Asn Pro Ile
 305 310 315 320
 Lys Lys Gln Ile Leu Leu Phe Ala Val Ala Ser Glu Ser Thr Lys Phe
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 Asp Tyr Phe Gly Ile Thr Gly Gln Glu Thr Thr Val Leu Ala Tyr Thr
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 Gly Asn Glu Asp Ala Arg Lys Phe Phe Leu Asp Gly Glu Val Ser Leu
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 Pro Phe Tyr Lys Ser Glu Pro Val Pro Glu Ser Asn Asp Gly Asp Val
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 Lys Ile Val Val Gly Lys Asn Leu Asp Leu Ile Val Phe Asp Glu Thr
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Lys Asp Val Leu Leu Glu Ile Tyr Ala Pro Trp Cys Gly His Cys Gln
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Ser Leu Glu Pro Thr Tyr Asn Asn Leu Ala Lys His Leu Arg Ser Val
465 470 475 480

Asp Ser Leu Val Val Ala Lys Met Asp Gly Thr Thr Asn Glu His Pro
485 490 495

Arg Ala Lys Ser Asp Gly Tyr Pro Thr Ile Leu Phe Tyr Pro Ala Gly
500 505 510

Lys Lys Ser Phe Glu Pro Ile Thr Phe Glu Gly Glu Arg Thr Val Val
515 520 525

Asp Leu Tyr Lys Phe Ile Lys Lys His Ala Ser Ile Pro Phe Lys Leu
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Ser Ser Gly Thr Asn Ser Lys Asp Glu Leu
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Ala Arg Val Glu Met Asp Asn Glu Asp Val Gly Lys Pro Val Ser Glu
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Tyr Phe Gly Ile Ser Gly Asn Ala Pro Lys Val Leu Gly Tyr Thr Gly
20 25 30

Asn Asp Asp Gly Lys Lys Phe Val Leu Asp Gly Glu Val Thr Thr Asp
35 40 45

Lys Ile Lys Ala Phe Gly Glu Asp Phe Val Glu Asp Lys Leu Lys Pro
 50 55 60
 Phe Tyr Lys Ser Asp Pro Val Pro Glu Ser Asn Asp Gly Asp Val Lys
 65 70 75 80
 Ile Val Val Gly Asn Asn Phe Asp Glu Ile Val Leu Asp Glu Ser Lys
 85 90 95
 Asp Val Leu Leu Glu Ile Tyr Ala Pro Trp Cys Gly His Cys Gln Ser
 100 105 110
 Leu Glu Pro Ile Tyr Asn Lys Leu Ala Lys His Leu Arg Asn Ile Asp
 115 120 125
 Ser Leu Val Ile Ala Lys Met Asp Gly Thr Thr Asn Glu His Pro Arg
 130 135 140
 Ala Lys Pro Asp Gly Phe Pro Thr Leu Leu Phe Phe Pro Ala Gly Asn
 145 150 155 160
 Lys Ser Phe Asp Pro Ile Thr Val Asp Thr Asp Arg Thr Val Val Ala
 165 170 175
 Phe Tyr Lys Phe Leu Lys Lys His Ala Ser Ile Pro Phe Lys Leu Gln
 180 185 190
 Lys Pro Thr Ser Thr Ser Glu Ser Asp Ser Lys Gly Ser Ser Asp Ala
 195 200 205
 Lys Glu Ser Gln Ser Ser Asp Val Lys Asp Glu Leu
 210 215 220

<210> 13
 <211> 1126
 <212> DNA
 <213> Glycine max

<400> 13
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 ttgaaactct tcaagatgtt gcaaaaacat tcaagtcaaa gataatgttt atatatgtgg 180
 atattaatga tgagaacctt gcaaagccct tcttaacatt gtttgggtctt gaagaatcaa 240
 aaaatactgt ggtcgccgca ttgataatg caatgagctc aaaatatttg ttggagacaa 300
 aaccaacaca aagcaatatt gaagagttct gcaataacct tgtgcaaggg tctttgtcac 360
 cttacttcaa gtcacagcca attccagata atacagaatc aagtgtccat gttattgtcg 420
 ggaaaacatt tgatgatgaa atcttgagca gcgagaagga tgtgctcttg gaggtattta 480
 cgccttggtg catcaactgt gaggccacta gcaagcaagt agagaagttg gcaaagcact 540
 acaaaggatc aagtaattcta atatttgcaa ggatagatgc ttcagcaaatt gaacatccaa 600
 aactgcaagt gaatgactac cccacgcttc tactttacag agcagacgat aaggcaaattc 660
 cgatcaaaact ttccacaaaa tctagtttga aagagttggc tgcattccatt aacaaatattg 720
 taaaagtcaa gaatcaagtc gtcaaagatg agttatgaa catatcaaaa agttttggga 780
 gaaaacact taacctgaa gaaagtaaaa cattatggaa agaaacaaat attattgtgt 840
 cttgctgaag ctttttctaa tttttattaa cctttccctt gccattttat ggtggtccaa 900
 atatgagtta gtctattatt atttgagtta gcttactgct aaattgcgaa agctagtcaa 960
 attataacat gtaatgaact acagaacata cttgatacac caaacattgt accgatcaac 1020
 actttccatt tgcattctcat agaaacctgc aaatcacagg cttaaagttg atgcattgac 1080
 acatatcaaa ctcaagcttt tataattcga aaaaaaaaaa aaaaaa 1126

<210> 14
 <211> 251
 <212> PRT
 <213> Glycine max

 <400> 14
 Thr Ser Lys Phe Pro Leu Val Thr Lys Leu Thr Glu Met Asn Ser Ile
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 Arg Val Tyr Ser Ser Pro Ile Lys Leu Gln Val Leu Val Phe Ala Asn
 20 25 30
 Ile Asp Asp Phe Lys Asn Leu Leu Glu Thr Leu Gln Asp Val Ala Lys
 35 40 45
 Thr Phe Lys Ser Lys Ile Met Phe Ile Tyr Val Asp Ile Asn Asp Glu
 50 55 60
 Asn Leu Ala Lys Pro Phe Leu Thr Leu Phe Gly Leu Glu Glu Ser Lys
 65 70 75 80
 Asn Thr Val Val Ala Ala Phe Asp Asn Ala Met Ser Ser Lys Tyr Leu
 85 90 95
 Leu Glu Thr Lys Pro Thr Gln Ser Asn Ile Glu Glu Phe Cys Asn Asn
 100 105 110
 Leu Val Gln Gly Ser Leu Ser Pro Tyr Phe Lys Ser Gln Pro Ile Pro
 115 120 125
 Asp Asn Thr Glu Ser Ser Val His Val Ile Val Gly Lys Thr Phe Asp
 130 135 140
 Asp Glu Ile Leu Ser Ser Glu Lys Asp Val Leu Leu Glu Val Phe Thr
 145 150 155 160
 Pro Trp Cys Ile Asn Cys Glu Ala Thr Ser Lys Gln Val Glu Lys Leu
 165 170 175
 Ala Lys His Tyr Lys Gly Ser Ser Asn Leu Ile Phe Ala Arg Ile Asp
 180 185 190
 Ala Ser Ala Asn Glu His Pro Lys Leu Gln Val Asn Asp Tyr Pro Thr
 195 200 205
 Leu Leu Leu Tyr Arg Ala Asp Asp Lys Ala Asn Pro Ile Lys Leu Ser
 210 215 220
 Thr Lys Ser Ser Leu Lys Glu Leu Ala Ala Ser Ile Asn Lys Tyr Val
 225 230 235 240
 Lys Val Lys Asn Gln Val Val Lys Asp Glu Leu
 245 250

 <210> 15
 <211> 1943
 <212> DNA
 <213> Glycine max

40

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<400> 15
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ctcgacgagc cctccgccgc gccggagcac ggccactacc acgacgatga cgccaatttc 180
ggcgacttcg aggaggaccc ggaggcgtag aagcagcccg aggtggacga gaaggacgtc 240
gtcattttga aggagaagaa cttcaccgac accgtcaaga gcaaccgctt cgtcatggtc 300
gagttctacg cgccctgggtg cggccactgc caggccctcg cgccggagta cgccgccgcc 360
gcgacggaac tcaagggcga agacgtaatt ttggcaaagg tggatgccac cgaggagaat 420
gaattggcgc agcagtacga tgttcagggt tccccactg tccacttctt cgttgatggc 480
attcacaagc cttataatgg ccaaaggacc aaagatgcta tagtgacgtg gataggaaag 540
aagatcggac ctggcatata caacttgact acagtggagg atgctcaacg catcttgacc 600
aacgaaacta aagttgtttt gggcttcctc aactctttag ttggctcctga gagtggagg 660
cttgctgctg cttcaagact tgaggatgat gtcaattttt atcaaactgt ggatcctgat 720
gtggcaaagc ttttccatat tgaccagat gttaagcgcc cagctttgat cctcgtcaag 780
aaagaggagg aaaaacttaa ccactttgat ggcaaatttg agaagtcgga aatagcagac 840
tttgtcttct ccaacaagct tcctttggta acaattttta caagagaaaag tgccccatca 900
gtcttcgaaa atccaatcaa gaaacagttg ttgctgtttg caacttcaaa tgattcagag 960
aagttgatcc ctgcatttaa agaagctgca aaatctttca agggaaagtt gatctttgta 1020
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gggaatgctc caaaagtact tgggtacact gggaatgatg atggaaaaaa atttgtgctt 1140
gatggagagg tgactgctga caaaattaag cagtttgggg acgatttcct tgaagacaag 1200
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aagtgatata tttttattta ttgaaactga ttcagacaga tgatgacatg gtgactgagg 1740
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aggagacaaa tgcgaggcac atatgtatta ctattaactt aaatttttac aactgggcat 1860
tttagaattt tgggttgaga cttcaataaa ttccccctta aattttaaaa aaaaaaaaaa 1920
aaaaaaaaaac tcgagactag ttc 1943

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<210> 16
<211> 551
<212> PRT
<213> Glycine max

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<400> 16
Met Arg Ile Leu Val Val Leu Ser Leu Ala Thr Leu Leu Leu Phe Ser
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Ser Leu Phe Leu Thr Leu Cys Asp Asp Leu Thr Asp Asp Glu Asp Leu
      20             25             30

Gly Phe Leu Asp Glu Pro Ser Ala Ala Pro Glu His Gly His Tyr His
      35             40             45

Asp Asp Asp Ala Asn Phe Gly Asp Phe Glu Glu Asp Pro Glu Ala Tyr
      50             55             60

Lys Gln Pro Glu Val Asp Glu Lys Asp Val Val Ile Leu Lys Glu Lys
      65             70             75             80

Asn Phe Thr Asp Thr Val Lys Ser Asn Arg Phe Val Met Val Glu Phe
      85             90             95

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Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Ala Pro Glu Tyr Ala
 100 105 110
 Ala Ala Ala Thr Glu Leu Lys Gly Glu Asp Val Ile Leu Ala Lys Val
 115 120 125
 Asp Ala Thr Glu Glu Asn Glu Leu Ala Gln Gln Tyr Asp Val Gln Gly
 130 135 140
 Phe Pro Thr Val His Phe Phe Val Asp Gly Ile His Lys Pro Tyr Asn
 145 150 155 160
 Gly Gln Arg Thr Lys Asp Ala Ile Val Thr Trp Ile Gly Lys Lys Ile
 165 170 175
 Gly Pro Gly Ile Tyr Asn Leu Thr Thr Val Glu Asp Ala Gln Arg Ile
 180 185 190
 Leu Thr Asn Glu Thr Lys Val Val Leu Gly Phe Leu Asn Ser Leu Val
 195 200 205
 Gly Pro Glu Ser Glu Glu Leu Ala Ala Ala Ser Arg Leu Glu Asp Asp
 210 215 220
 Val Asn Phe Tyr Gln Thr Val Asp Pro Asp Val Ala Lys Leu Phe His
 225 230 235 240
 Ile Asp Pro Asp Val Lys Arg Pro Ala Leu Ile Leu Val Lys Lys Glu
 245 250 255
 Glu Glu Lys Leu Asn His Phe Asp Gly Lys Phe Glu Lys Ser Glu Ile
 260 265 270
 Ala Asp Phe Val Phe Ser Asn Lys Leu Pro Leu Val Thr Ile Phe Thr
 275 280 285
 Arg Glu Ser Ala Pro Ser Val Phe Glu Asn Pro Ile Lys Lys Gln Leu
 290 295 300
 Leu Leu Phe Ala Thr Ser Asn Asp Ser Glu Lys Leu Ile Pro Ala Phe
 305 310 315 320
 Lys Glu Ala Ala Lys Ser Phe Lys Gly Lys Leu Ile Phe Val Tyr Val
 325 330 335
 Glu Met Asp Asn Glu Asp Val Gly Lys Pro Val Ser Glu Tyr Phe Gly
 340 345 350
 Ile Ser Gly Asn Ala Pro Lys Val Leu Gly Tyr Thr Gly Asn Asp Asp
 355 360 365
 Gly Lys Lys Phe Val Leu Asp Gly Glu Val Thr Ala Asp Lys Ile Lys
 370 375 380
 Ala Phe Gly Asp Asp Phe Leu Glu Asp Lys Leu Lys Pro Phe Tyr Lys
 385 390 395 400
 Ser Asp Pro Val Pro Glu Ser Asn Asp Gly Asp Val Lys Ile Val Val
 405 410 415

Gly Asn Asn Phe Asp Glu Ile Val Leu Asp Glu Ser Lys Asp Val Leu
420 425 430

Leu Glu Ile Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Glu Pro
435 440 445

Ile Tyr Asp Lys Leu Ala Lys His Leu Arg Asn Ile Glu Ser Leu Val
450 455 460

Ile Ala Lys Met Asp Gly Thr Thr Asn Glu His Pro Arg Ala Lys Pro
465 470 475 480

Asp Gly Phe Pro Thr Leu Leu Phe Phe Pro Ala Gly Asn Lys Ser Phe
485 490 495

Asp Pro Ile Thr Val Asp Thr Asp Arg Thr Val Val Ala Phe Tyr Lys
500 505 510

Phe Leu Lys Lys His Ala Ser Ile Pro Phe Lys Leu Gln Lys Pro Thr
515 520 525

Ser Thr Ser Asp Ala Lys Gly Ser Ser Asp Ala Lys Glu Ser Gln Ser
530 535 540

Ser Asp Val Lys Asp Glu Leu
545 550

<210> 17
<211> 1565
<212> DNA
<213> Triticum aestivum

<400> 17
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cagctcatgc cgcggttcgc cgaggccgcc gccgcgctgc gcgccatggg cagcgccgctc 120
gccttcgcga agctcgacgg ggagcgctac cccaaggcgg ctgccgccgt cgggggtcaag 180
ggcttcccca ccgtgctcct cttcgtcaat ggcaaccgagc acgcctacca tggcctccac 240
accaaggacg ccatagttag ttgggtaaga aagaaaactg gcgagccaat cattaggctt 300
cagtctaagg attcagctga ggagttcctc aaaaaggaca tgacctttgt tattgggcta 360
ttcaagaatt ttgaggagc agaccatgaa gaatttgtga aggcagcaac cacagacaac 420
gaggtacagt ttgtagaaac cagtatacga cgtgttgcca aagttctatt tccaggtatt 480
acgtccgagg agaaatttgt gggcctcggt aaaagcgagc cagagaagtt tgaaaagttc 540
gatgggaaat ttgaagaaac ggaaattctg cggtttgttg agctcaacaa gtttcctcta 600
attactgtat tcactgagct caattccggt aaagtatatt caagccctat taagctacag 660
gtcttcacct ttgcagaggc ttatgatttt gaagatcttg aatctatggt tgaagaaata 720
gccagagcat tcaagacaaa gataatgttt atatatgttg aactgctga agaaaacctt 780
gcaaaaccat tctcactctt ttatggcctt gaatcagaaa aaaagcctac tgttacagca 840
tttgatacaa gcaatggagc caagtatctg atggaggcag atatcaatgc aaacaacctg 900
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gcgataagta aaaatgttga gaagttggcg aagcatttca gtggttcgga caatcttaaa 1140
tttgacgca tagatgcttc tgtgaatgaa catcccaaat tgaagggtgaa taattccccg 1200
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ctttattcgc gtgctgtgtt aagttgacta aagtcaatgg tatataatat aggtacctaa 1500
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aaaaa 1565

<210> 18
 <211> 451
 <212> PRT
 <213> Triticum aestivum

<400> 18
 Ala Arg Asp His Ala Glu Leu Leu Leu Leu Gly Tyr Ala Pro Trp Cys
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 Glu Arg Ser Ala Gln Leu Met Pro Arg Phe Ala Glu Ala Ala Ala Ala
 20 25 30
 Leu Arg Ala Met Gly Ser Ala Val Ala Phe Ala Lys Leu Asp Gly Glu
 35 40 45
 Arg Tyr Pro Lys Ala Ala Ala Val Gly Val Lys Gly Phe Pro Thr
 50 55 60
 Val Leu Leu Phe Val Asn Gly Thr Glu His Ala Tyr His Gly Leu His
 65 70 75 80
 Thr Lys Asp Ala Ile Val Thr Trp Val Arg Lys Lys Thr Gly Glu Pro
 85 90 95
 Ile Ile Arg Leu Gln Ser Lys Asp Ser Ala Glu Glu Phe Leu Lys Lys
 100 105 110
 Asp Met Thr Phe Val Ile Gly Leu Phe Lys Asn Phe Glu Gly Ala Asp
 115 120 125
 His Glu Glu Phe Val Lys Ala Ala Thr Thr Asp Asn Glu Val Gln Phe
 130 135 140
 Val Glu Thr Ser Asp Thr Arg Val Ala Lys Val Leu Phe Pro Gly Ile
 145 150 155 160
 Thr Ser Glu Glu Lys Phe Val Gly Leu Val Lys Ser Glu Pro Glu Lys
 165 170 175
 Phe Glu Lys Phe Asp Gly Lys Phe Glu Glu Thr Glu Ile Leu Arg Phe
 180 185 190
 Val Glu Leu Asn Lys Phe Pro Leu Ile Thr Val Phe Thr Glu Leu Asn
 195 200 205
 Ser Gly Lys Val Tyr Ser Ser Pro Ile Lys Leu Gln Val Phe Thr Phe
 210 215 220
 Ala Glu Ala Tyr Asp Phe Glu Asp Leu Glu Ser Met Val Glu Glu Ile
 225 230 235 240
 Ala Arg Ala Phe Lys Thr Lys Ile Met Phe Ile Tyr Val Asp Thr Ala
 245 250 255
 Glu Glu Asn Leu Ala Lys Pro Phe Leu Thr Leu Tyr Gly Leu Glu Ser
 260 265 270
 Glu Lys Lys Pro Thr Val Thr Ala Phe Asp Thr Ser Asn Gly Ala Lys
 275 280 285

Tyr Leu Met Glu Ala Asp Ile Asn Ala Asn Asn Leu Arg Glu Phe Cys
 290 295 300
 Leu Ser Leu Leu Asp Gly Thr Leu Pro Pro Tyr His Lys Ser Glu Pro
 305 310 315 320
 Leu Pro Gln Glu Lys Gly Leu Ile Glu Lys Val Val Gly Arg Thr Phe
 325 330 335
 Asp Ser Ser Val Leu Glu Ser His Gln Asn Val Phe Leu Glu Val His
 340 345 350
 Thr Pro Trp Cys Val Asp Cys Glu Ala Ile Ser Lys Asn Val Glu Lys
 355 360 365
 Leu Ala Lys His Phe Ser Gly Ser Asp Asn Leu Lys Phe Ala Arg Ile
 370 375 380
 Asp Ala Ser Val Asn Glu His Pro Lys Leu Lys Val Asn Asn Ser Pro
 385 390 395 400
 Thr Leu Phe Leu Tyr Leu Ala Glu Asp Lys Asn Asn Pro Ile Lys Leu
 405 410 415
 Ser Lys Lys Ser Ser Val Lys Asp Met Ala Lys Leu Ile Lys Glu Lys
 420 425 430
 Leu Gln Ile Pro Asp Val Glu Thr Val Ala Ala Pro Asp Asn Val Lys
 435 440 445
 Asp Glu Leu
 450

<210> 19
 <211> 1078
 <212> DNA
 <213> Triticum aestivum

<400> 19
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 tcaccaccct cacacaggag accgcccctg cgattttcga taatccgatc aagaagcaaa 120
 ttttgctgtt tgctgttgcg aaggagtcct caaaatttct gcccatcatt aaggaaacag 180
 caaaatcatt caaggggaag cttttatttg tctttgtgga gcgtgacaat gaggaagttg 240
 gcgaacctgt tgccaattac tttggaatta ctggacaaga gaccacggtt cttgcttaca 300
 ctgggaatga agacgctaag aagttcttct tcaccggtga aatatcactg gacaccatta 360
 aggaatttgc tcaagatttc atggaggaca agctcacacc atcctacaag tctgaccag 420
 tacctgaatc caatgatgag gacgtcaaag ttgttggttg caagagtcta gatcaaatag 480
 ttctggatga gtcaaaggat gtccttttgg agatatatgc gccatggtgt ggccattgtc 540
 agtcactgga gcctatctac aacaagctgg ccaagtacct ccgtggcatc gactcccttg 600
 taatagccaa aatggacggc acaacaatg agcatcctcg tgccaagccc gatgggttcc 660
 ccacgatact cttctaccca gctgggaaga aaagctttga gcctataact ttcgaggggg 720
 gccggacagt ggtagagatg tacaagttcc tcaagaagca tgccgccatc cctttcaagc 780
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 tcaaccaacc ttggctgctg caagtgtatg ctgacaacac aaatatatac tgctgtagaa 1020
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45

<210> 20
 <211> 294
 <212> PRT
 <213> Triticum aestivum

<400> 20
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 20 25 30
 Asp Asn Pro Ile Lys Lys Gln Ile Leu Leu Phe Ala Val Ala Lys Glu
 35 40 45
 Ser Ser Lys Phe Leu Pro Ile Ile Lys Glu Thr Ala Lys Ser Phe Lys
 50 55 60
 Gly Lys Leu Leu Phe Val Phe Val Glu Arg Asp Asn Glu Glu Val Gly
 65 70 75 80
 Glu Pro Val Ala Asn Tyr Phe Gly Ile Thr Gly Gln Glu Thr Thr Val
 85 90 95
 Leu Ala Tyr Thr Gly Asn Glu Asp Ala Lys Lys Phe Phe Phe Thr Gly
 100 105 110
 Glu Ile Ser Leu Asp Thr Ile Lys Glu Phe Ala Gln Asp Phe Met Glu
 115 120 125
 Asp Lys Leu Thr Pro Ser Tyr Lys Ser Asp Pro Val Pro Glu Ser Asn
 130 135 140
 Asp Glu Asp Val Lys Val Val Val Gly Lys Ser Leu Asp Gln Ile Val
 145 150 155 160
 Leu Asp Glu Ser Lys Asp Val Leu Leu Glu Ile Tyr Ala Pro Trp Cys
 165 170 175
 Gly His Cys Gln Ser Leu Glu Pro Ile Tyr Asn Lys Leu Ala Lys Tyr
 180 185 190
 Leu Arg Gly Ile Asp Ser Leu Val Ile Ala Lys Met Asp Gly Thr Asn
 195 200 205
 Asn Glu His Pro Arg Ala Lys Pro Asp Gly Phe Pro Thr Ile Leu Phe
 210 215 220
 Tyr Pro Ala Gly Lys Lys Ser Phe Glu Pro Ile Thr Phe Glu Gly Gly
 225 230 235 240
 Arg Thr Val Val Glu Met Tyr Lys Phe Leu Lys Lys His Ala Ala Ile
 245 250 255
 Pro Phe Lys Leu Lys Arg Pro Asp Ser Ser Ala Ala Arg Thr Asp Ser
 260 265 270
 Ala Glu Gly Pro Gly Ser Thr Thr Asp Ser Glu Lys Ser Ser Gly Ser
 275 280 285

[illegible]